Chapter-II

Concept, Nature and Scope of DNA Technology –Scientific, Social and Legal Study

1. Introduction:

This chapter deals with definitions and meaning of legal and scientific terms and their use and importance in today's parlance.

1.1 Basic Biology of DNA

DNA is the abbreviation for deoxyribonucleic acid, which is the genetic material present in the cells of all living organisms. DNA is the fundamental building block for an individual's entire genetic makeup. A person's DNA is the same in every cell (with a nucleus). The DNA in a person's blood is the same as the DNA in their skin cells, semen, and saliva.

DNA is comprised of four building blocks called bases. The building blocks are: Cytosine, Guanine, Thymine, and Adenine. These are commonly referred to as C, G, T, A. It is the order (sequence) of these building blocks that determines each person's genetic characteristics[13].

DNA is contained in blood, semen, skin cells, tissue, organs, muscle, brain cells, bone, teeth, hair, saliva, mucus, perspiration, fingernails, urine, feces, etc.

Formation of DNA:

Every cell in the human body contains a nucleus, with the exception of red blood cells, which lose this structure as they mature. Within the nucleus are tightly coiled threadlike structures known as chromosomes. Humans normally have 23 pairs of chromosomes, one member of each pair derived from the mother and one from the father. One of those pairs consists of the sex chromosomes – with two X

[13]See, Article on DNA Technology, Available at http://www.dna.gov/basics/biology (Last accessed on: 3rd Jan., 2007)

chromosomes determining femaleness, and one X and one Y determining maleness. The other 22 chromosomes are known as autosomes.

Each chromosome has within it, arranged end-to-end, hundreds or thousands of genes, each with a specific location, consisting of the inherited genetic material known as deoxyribonucleic acid (DNA). Scientists have numbered these autosomes from 1 – 22 in size order, with chromosome 1 being the largest (containing nearly 3,000 genes).

DNA contains a code that directs the 'expression' or production of proteins, which form much of the structure of the cell and control the chemical reactions within them. The DNA of each gene is characterized by a unique sequence of bases that form the 'genetic code'. These bases are arranged in groups of three, known as codons or phrases[14].

The base sequence is the crucial feature of the gene. It is this sequence that carries the genetic information essential for the synthesis of an RNA molecule that may subsequently direct the synthesis of a protein molecule or may itself be functional in the cell. This process is called gene expression; it has two stages. The first stage in gene expression is transcription (the process by which RNA directs the synthesis of a protein). Proteins are composed of amino acids and are the molecules that carry out the work of the cell[15].

There are four basic building blocks (referred to as bases or nucleotides) for DNA: Adenine (A) and Guanine (G), which is known as Purines; and Thymine (T) and Cytosine (C), which are known as Pyramids.

These nucleotides link together to form long polynucleotide chains, having a defined sequence of nucleotides.

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[14]See, Article on DNA Technology, Available at http://www.dna.gov/basics/biology (Last accessed on: 3rd Jan., 2007)

15See, Article "The Ethics of Patenting DNA, a Discussion" , Presented in Nuffield Council on Bioethics 2002, Available at http://www.nuffieldbioethics.org/patenting-dna (Last accessed on: 13th Jan., 2007)

A DNA molecule consists of two of these chains, linked together by hydrogen bonds, running in opposite directions. The two chains link together in a ladder-like shape, twisted into the now famous double helix [16].

Linkage of the chains follows a strict rule, known as complementary base pairing, so that the base A can only pair with the base T, and vice versa; and the base G can only pair with the base C, and vice versa. The human genome is comprised of about 3.2 billion of these base pairs.

A genome is an organism's entire genetic material. All living organisms contain genetic material or genomes. One of the most commonly accepted definitions of gene is that a gene contains all of the information required to determine the expression of a specific protein or chain of amino acid (a polypeptide). Sometimes a polypeptide can form a complete protein on its own (as in the case of insulin), but in most cases a number of polypeptides combine to create a single protein (as in the case of collagen and globin)[17].

Proteins are critical components of all cells, determining color, shape and function. Proteins can have a structural role (such as keratin, from which hair is made), or a functional role in regulating the chemical reactions that occur within each cell (such as the enzymes involved in producing energy for the cell). Proteins are themselves made up of a chain of amino acids. Within the DNA there is a code that determines which amino acids will come together to form that particular protein.

The genetic code for each amino acid, consisting of three bases, is virtually identical across all living organisms. Different genes are switched on and off in different cells, leading to different proteins being made or expressed with varying structures, appearances and functions – leading to the production of brain cells, nerve cells, blood cells, and so on. Contemporary stem cell research is based on the idea that it should be possible to learn how to use gene switches to coax stem cells into developing into the specialized cells or tissue needed for therapeutic purposes. When

[16] first described by James Watson and Francis Crick in 1953, who were awarded the Nobel Prize for their work "'A Structure for Deoxyribose Nucleic Acid' (1953) 171 Nature 737

[17] See Article on DNA Technology, Available at http://www.dna.gov/basics/biology (Last accessed on: 3rd Jan., 2007)

the instructions in a gene are to be read, the DNA comprising that gene unwinds and the two strands of the double helix separate.

An enzyme called RNA polymerase allows a complementary copy of one strand of the DNA to be made. This copy is made from RNA nucleotides, and is called messenger RNA (or mRNA) because it carries the coded genetic information to the protein-producing units in the cell, called ribosomes.

This process of reading the message in the DNA is called transcription. In the ribosome, the amino acids are assembled in the precise order coded for in the mRNA. The process of converting the message encoded in the RNA (mRNA) to protein using the ribosome is called translation. When the whole message has been translated, the long chain of amino acids folds itself up into a distinctive shape that depends upon its sequence – and is then known as a protein. In humans, genes comprise only a small proportion of the DNA in a cell. Up to 98% of DNA consists of 'non-coding' regions – popularly, but incorrectly, referred to as 'junk DNA' – which are full of repeat sequences (micro-satellites), pseudogenes and retroviruses. By way of contrast, there are no non-coding portions of DNA in bacteria – there are only genes, each one expressing a specific protein[18].

In recent years, genetic scientists increasingly have come to believe that non-coding DNA may be the basis for the complexity and sophistication of the human genome, which permits only 30,000 or so genes to produce about 200,000 proteins. A leader in this field, Professor John Mattick, Director of the Institute for Molecular Biology at the University of Queensland, has surmised that non-coding DNA forms a massive parallel processing system producing secondary signals that integrate and regulate the activity of genes and proteins.

In effect, they co-ordinate complex programs involved in the development of complex organisms. According to recent estimates , all humans have the same basic set of about 30,000 – 35,000 genes, which is far lower than the early estimates of 200,000 (based on the number of proteins), and even the relatively recent estimates of 100,000 used at the start of Human Genome Project.

[18]Ibid 1

Genes may come in different versions, known as alleles. These alleles arise when there is a change in the ordering of the bases (nucleotides) described above – in effect, a 'typographical error' in the code, involving the change of a single letter, the inversion of two letters, the deletion or insertion of a codon, or the repetition of a codon. This change in the sequence (a mutation) may cause no harm, merely resulting in a polymorphism, or it may make the gene faulty in the way it directs (expresses) the production of protein. In a very few cases the mutation is beneficial. Although any two human beings are at least 99.9% genetically identical, the precise DNA sequence of about 3.2 billion base pairs will differ slightly in each person's genetic code. The 0.1% of difference is thought to compromise more than 10 million common single letter genetic variations (single nucleotide polymorphisms, or SNPs) as well as a larger number of rare variants. The rate of variation is very low in humans (one SNP per 1,300 bases) compared with other species, including other primates – suggesting a population that has descended from a small 'starter population'. This explains both the striking similarities among all people, which are the result of our common inheritance, and the many individual differences found even within a nuclear family.

Mutations are permanent and inheritable changes in the ability of a gene to encode its protein. Much like typographical errors, which can change the meaning of a word, or even render a sentence as gibberish, such changes in gene structure can have severe effects on the ability of a gene to encode its protein. Some mutations prevent any protein from being produced, some produce a non-functional or only partially functional protein, and some produce a faulty or poisonous version of the protein.

The unique combination of alleles found in a particular individual's genetic make-up is said to constitute that person's genotype. The observable physical characteristics of this genotype, as determined by the interaction of both genetic makeup and environmental factors, is said to constitute that person's phenotype. This includes features such as color of eye and hair, determined genetically, as well as height and weight – determined by genetic factors as well as by diet, access to proper healthcare and other environmental influences.

Because mutations can affect the functioning and expression of the alleles of genes, resulting in particular traits or characteristics, it is possible to follow the pattern of

inheritance of the different alleles of a gene in a family. For most genes, two copies are found in an individual.

If the two copies are the same allele, the individual is said to be homozygous. If two different alleles for that gene are present, the individual is referred to as heterozygous for that gene – except for those traits coded for by genes that are found on the X chromosome. A dominant trait is one that is manifested when a person has only one mutated allele in a particular gene pair. An affected person may have inherited the mutated allele from either parent or, as the result of a new mutation, may be the first person in the family to have it. There is one-in-two chance that a child will inherit a genetic trait if one parent has a dominant mutated allele[19].

Examples of autosomal dominant traits include HD, myotonic dystrophy, hereditary non-polyposis colorectal cancer, Marfan syndrome, familial adenomatous polyposis, and early onset familial Alzheimer's disease.

Medical conditions or diseases linked to genes can be classified in a number of ways, including: monogenic (or single gene) disorders; polygenic (or multi-gene) disorders; and multifactorial disorders. A monogenic disorder is one in which a mutation in one or both alleles of a single gene is the main factor in causing a genetic disease. Much of our early understanding about genetic influences on health is derived from the observation and study of monogenic disorders such as Huntington's disease (a neurodegenerative disease which is inherited in an autosomal dominant pattern) – although such diseases are relatively rare.

The vast majority of medical conditions with some genetic link involve either the complex interaction of a number of genes (polygenic) or the complex interaction between genes and the environment (multifactor disorders). In the case of multifactor disorders, inheriting a mutated allele for a particular condition means that a person is susceptible or predisposed to develop the condition. Other factors such as diet or exposure to certain environmental factors are necessary to bring about the expression of the trait or condition.

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[19] Ibid 1

Most of the important and common medical problems in humans are multifactor, including heart disease, hypertension, psychiatric illness (such as schizophrenia), dementia, diabetes, and cancers. According to the Human Genome Database, as on 29 December 2002, 14,014 genes had been mapped to individual chromosomes, of which 1,639 had been identified as being involved in a genetic disorder. It may be that most of the simple linkages have already been made, since the rate of discovery has slowed dramatically despite better technology; of the last 3,783 genes to be mapped, only 17 have been identified with a genetic disorder.

2. DNA Fingerprinting:

DNA Fingerprinting is a method where, a person's genetic traits, genes, are used to make specific strings of DNA letters that are cut into patterns of shorter strings separated by length these banding patterns can identify a unique human being.

Forensic scientists are able to "read" the DNA sequences and find differences among species. They reduce the base names down to letters, namely "a", "c", "t" and "g". Then scientists read the sequence of these letters by looking at one-half of the ladder. Although the majority, 99.9% of the letter sequence on a human DNA strand is identical, there are portions of each strand that differ from individual to individual. Thus, in a DNA strand with three billion letters, one tenth of one percent difference translates into three million separate spelling differences. These are differences that scientists examine in the process known as DNA fingerprinting to determine identity and heritage.

Unfortunately, for purposes of forensic DNA fingerprinting, scientists do not read all three billion letters. Instead, to save time and money, scientists look at a very small handful of sites of variation. Along the DNA strand, or genome, there are regions where the base pair sequences repeat themselves. For instance, one person could have the sequence of "t-a-c-t-g" repeat three times and another person could have that same sequence repeat twice or appear only once. Thus, these normally biologically insignificant sequence repetitions create spelling difference in particular areas. In general, forensic scientists cut the DNA strands with an enzyme at these points of repetition. They then record the repetition variations by reducing the data into a bar code type expression. When comparing DNA samples from crime scene evidence to a

suspect's DNA sample, scientists will compare the "bar code" information from each site of variation. If the bar code differs between the evidence and the suspect's DNA at any point, that particular suspect is usually ruled out as a possible source of the DNA evidence. However, if the bar codes are the same along all points of variation tested, the suspect is considered more likely to have left the evidence. It is important to note, however, that this does not mean the suspect committed the crime or even left the DNA evidence. Because scientists do not read the entire DNA, looking for any and all variations, two samples conceivably could appear as exact matches but actually may differ in some other portion of the strand.

Some courts have rejected the use of the term "DNA Fingerprinting". Because-

(1) It tends to trivialize the intricacies of the processes by which information for DNA comparisons is obtained to the process of fingerprinting, and

(2) The word fingerprinting tends to suggest erroneously that DNA testing of the type involved in this case will identify conclusively, like real fingerprinting, the one person in the world who could have left the identifying evidence at the crime scene.

DNA profiles differ from conventional fingerprints in the following respects:

- DNA holds vastly more information than fingerprints.
- DNA profile can be used in establishing kinship relations.
- The sample from which the profile was obtained may hold predictive health and other information of a sensitive nature.
- As genetic information is shared with biological relatives, an individual's profile might indirectly implicate a relative in an offence.
- DNA can be amplified from tiny and aged samples and may be recovered from almost any cell or tissue unlike fingerprinting.

3. Various Techniques of DNA Fingerprinting:

DNA testing technology has developed three main types of DNA testing that are widely used for both science and legal identification purposes. The circumstances,

such as the age, size, and handling of the sample, determine what type of testing is to be used[20].

3.1 Restriction Fragment Length Polymorphism Testing (RFLPT)

It is widely used for legal identification purposes by forensic scientists. This procedure was developed by Professor Sir Alec Jeffreys and is generally accepted by the courts in the Unites States and has resulted in a number of post-conviction exonerations. This testing process does not actually "read" the sequence repetitions, but it isolates certain areas of repetition and essentially measures the length of these sections, which are then recorded as bar codes and compared between samples.

RFLP Testing is best used on large, unadulterated or untarnished samples and when it is possible; it is very discriminate, leading to statistically strong exclusions and inclusions even when only testing a few DNA regions.

3.2 VNTR Typing (Variable number Tandem Repeats)

Certain regions of DNA, known as *variable number tandem repeats* (VNTRs), have no known function and show great variability among individuals. These are the regions of the DNA used in VNTR typing. The VNTR loci used in forensic tests reside on different chromosomes (or sometimes very far apart on the same chromosome), so they are independently inherited.

In VNTR regions, usually ranging from 500 to 10,000 nucleotide pairs, a core sequence of some 15-35 base pairs repeats many times consecutively along the chromosome. The number of repeats varies from person to person. (Sequences with different numbers of repeated units are called *alleles*, even though the word originally applied to functional genes.

Several features of VNTR regions make them useful for forensic testing and identification. First, VNTR loci have a very large number of alleles (often a hundred or more), and none of the alleles is very common, so great variation exists among individuals. Second, because VNTR regions have no known function, they are less

[20] Yashpal Singh and Mohammad Zaidi "*DNA Test in Criminal Investigation, Trial and Paternity Disputes*" , Alia Law Agency, Allahabad, 2006, p. 59

likely than functional genes to be influenced by natural selection and thus less likely to vary in the frequency with which they appear in different populations. Finally, the variable number of base sequence repeats makes VNTR regions identifiable by their lengths, so they can be readily sorted by laboratory procedures.

Although details vary somewhat among labs, the basic steps of VNTR typing are uniform. In VNTR typing, the lab first excises fragments of chromosomes that begin and end with certain sequences of DNA base pairs from DNA at the crime scene and DNA from the suspect(s). The tester then measures the lengths of the DNA fragments in the samples by seeing how far they move through a slab of gelatinous material when attracted by an electric charge. The tester compares how far the sample fragments moved relative to how far fragments of known lengths moved. The analyst then applies a *"probe"* or genetic marker to make visible the genetic patterns at each locus. Commonly, labs examine four or five VNTR loci for each sample[21].

The following steps compose the typical VNTR analysis:

1) Isolate the DNA from the specimen to be examined;
2) Cut the DNA into discrete pieces using a bacterial enzyme (called a restriction enzyme);
3) Separate the different-sized DNA pieces using a process called gel electrophoresis;
4) Transfer the DNA from a gel to a nylon membrane to make it easier to work with;
5) Apply (or hybridize) a DNA probe to the membrane (the probe usually is radioactively labelled, although some labs are beginning to use luminescent molecules); and
6) Show the location of the probe, usually by exposing the membrane to x-ray film (autoradiography), or if luminescent probes are used, to light-sensitive film.

If a radioactive marker is used, the entire process for four or five probes takes several weeks.

After the film is developed, the analyst must examine the images and interpret the results of the test. The film typically shows a number of parallel bands running across it, like lanes on a highway. The position of each radioactively labelled band on the

[21] Yashpal Singh and Mohammad Zaidi ,"*DNA Test in Criminal Investigation, Trial and Paternity Disputes*" , Alia Law Agency, Allahabad, 2006, p. 64

membrane indicates the size of the VNTR. Because of measurement uncertainty, however, the test does not reveal the exact size of a band. The analyst must account for this uncertainty when analyzing autorads.

Because the most common DNA tests for measuring the lengths of the VNTR fragments are not sensitive enough to distinguish between fragments that are extremely close in size, laboratories group bands of similar size into *bins*. The analyst then treats the alleles within a bin as though they are a single allele. The usual width of a bin is about 10% of the mean (average) size of the VNTR segment at the centre of the bin. After binning, the analyst compares the number and location of the various bands in the lanes on the autorad. A person whose DNA falls into the same bin is said to be *homozygous*; while a person whose DNA falls into different bins is said to be *heterozygous*[22].

3.3. PCR-Polymerase Chain Reaction Testing-Nuclear DNA:

This elegant and simple process was developed by Kary B. Mullis-a Nobel Prize winner. PCR requires four nucleotide building blocks, inorganic chemicals, and a device to rapidly and accurately change and maintain the temperature for short period of time.- known as the thermal cycle.

In this process one or more specific small regions of the DNA are copied using DNA polymerase enzymes that a sufficient amount of DNA is generated from analysis. Very small or degraded specimens/biological samples are enough to under go the PCR technique. PCR technique is widely used for forensic identity purpose. This technique is generally used and relied upon by the scientific community and hence admissible in and accepted by court of laws.

This type of testing has become most widely used technique in the field of molecular biology and was first developed by Dr. Kary Mullis in 1984. PCR is also accepted by the courts and has led to a number of post-conviction exonerations. PCR testing can be done on smaller and less pristine samples. Small samples can be subjected to PCR testing because sample amplification is part of the process. Essentially, specific

[22] Yashpal Singh and Mohammad Zaidi ,"*DNA Test in Criminal Investigation, Trial and Paternity Disputes*" , Alia Law Agency, Allahabad, 2006, p. 66

regions of DNA are copied using an enzyme called Taq polymerase and then are compared in a type of bar code format. Like RFLP testing, exclusion is generally considered dispositive; however an inclusion is less discriminate. Therefore, in order to have a more statistically strong inclusion, PCR testing needs to be conducted at a number of sites along the DNA strand[23].

a. Steps of PCR Analysis:

In this three-step process, the lab first heats the double-stranded DNA segments to separate them into two strands. Second, the lab hybridizes the single-stranded segments with *primers*, short DNA segments that complement and define the target sequence to be amplified. Each primer serves as the starting point for replicating the target sequence when mixed with the enzyme DNA polymerase and the four-nucleotide building blocks (A, C, G and T). The process copies the complement of each of the separated stands, resulting in two double-stranded DNA segments. The lab then repeats the three-step cycle, usually twenty to thirty-five times[24].

Once the DNA is amplified, analysis precedes the same as with VNTR methods, with a few modifications. Like VNTR analysis, PCR-based methods rely on the principle of identifying different-sized fragments by their migration rates in an electric field.

b. Methods of PCR:

i. PCR-based methods are used on a number of different classes of DNA fragments and genes. One class of repeated DNA units labs analyze using PCR is *short tandem repeats* (STRs). These repeats of a few nucleotide units are very common and are distributed widely throughout the genome. While STRs have fewer alleles per locus than VNTRs, a very large number of loci are potentially usable.

ii. Another PCR application uses the DQA locus. Unlike VNTRs, the eight alleles at DQA code for a protein. Specific probes can distinguish six of the

[23] Yashpal Singh and Mohammad Zaidi ,"*DNA Test in Criminal Investigation, Trial and Paternity Disputes*" , Alia Law Agency, Allahabad, 2006,p. 69

[24] Yashpal Singh and Mohammad Zaidi ,"*DNA Test in Criminal Investigation, Trial and Paternity Disputes*" , Alia Law Agency, Allahabad, 2006, p. 78

eight alleles identified at this locus. The DQA system can be used, along with other markers, as part of a more detailed DNA profile.

iii. A third PCR system is the *Amplitype polymarker (PM)*. This system analyzes six loci simultaneously: DQA, *LDLR* (low-density lipoprotein receptor), *GYPA* (glycophorin A, the MN blood-groups), *HBGG* (hemoglobin gamma globin), D7S8 (an anonymous genetic marker on chromosome 7), and *GC* (group-specific component). Two or three distinguishable alleles exist at each locus. However, polymarker loci vary more among races than do VNTRs.

iv. Another PCR-based technique involves D1S80, a VNTR in which the largest allele is less than 1,000 base pairs long. The locus has a sixteen-base unit repeated a variable number of times. More than 30 distinguishable alleles exist at the locus, and the size classes are discrete. The analysis is complicated, however, by insertion or deletion of a single base.

v. Finally, another class of genetic marker is mitochondrial DNA. Unlike most DNA, which is found in the cell's nucleus, mitochondrial DNA is found outside the nucleus in the cell's mitochondria. Also unlike other DNA, mitochondrial DNA passes only from mother to child, so that all the children of one woman have identical mitochondrial DNA. Certain regions of the mitochondrial DNA are highly variable and thus have been used for forensic analysis. Because each person inherits mtDNA from his or her mother, the technique cannot distinguish siblings or other maternally related relatives[25].

c. Difference between PCR and VNTR:

PCR-based methods differ from VNTR analysis in several respects. First, PCR-based analyses usually permit exact identification of each allele, avoiding the problem of measurement uncertainty. Second, results of PCR-based analyses normally are available within about 24 hours, much sooner than VNTR results. Finally, PCR analysis is better suited than VNTR typing for smaller samples for which very little DNA are available.

[25] Yashpal Singh and Mohammad Zaidi ,"*DNA Test in Criminal Investigation, Trial and Paternity Disputes*" , Alia Law Agency, Allahabad, 2006, p., Alia Law Agency, Allahabad, 2006, p. 89

d. Disadvantages of PCR Method:

PCR analysis presents at least three disadvantages not present in VNTR analysis. First, a sample that is contaminated can make multiple copies of the wrong DNA. The amplification process is so efficient that a few stray molecules of contaminating DNA could affect the band pattern enough to cause an analyst to declare a no match when a match actually exists, or to declare a match when the evidence DNA actually does not match the suspect's DNA. Second, most markers used in PCR-based typing have fewer alleles than VNTRs, and the distribution of allele frequencies is not as flat. The lab therefore must analyze more loci to get the same amount of information about the likelihood that two people share a profile. Finally, some of the loci used in PCR-based analysis are functional genes; some are linked to important disease-producing genes. Recall that functional genes are more likely than non-functional markers to be influenced by natural selection and thus appear with different frequencies in different segments of the population (the sickle-cell example).

3.4 STR Analysis:

Short tandem repeat (STR) technology is a forensic analysis that evaluates specific regions (loci) that are found on nuclear DNA. The variable (polymorphic) nature of the STR regions that are analyzed for forensic testing intensifies the discrimination between one DNA profile and another. For example, the likelihood that any two individuals (except identical twins) will have the same 13-loci DNA profile can be as high as 1 in 1 billion or greater. [26]

Several genetic markers have been identified on the Y chromosome that can be used in forensic applications. Y-chromosome markers target only the male fraction of a biological sample. Therefore, this technique can be very valuable if the laboratory detects complex mixtures (multiple male contributors) within a biological evidence sample. Because the Y chromosome is transmitted directly from a father to all of his

[26] The Federal Bureau of Investigation (FBI)in U.S.A. has chosen 13 specific STR loci to serve as the standard for CODIS. The purpose of establishing a core set of STR loci is to ensure that all forensic laboratories can establish uniform DNA databases and, more importantly, share valuable forensic information. If the forensic or convicted offender CODIS index is to be used in the investigative stages of unsolved cases, DNA profiles must be generated by using STR technology and the specific 13 core STR loci selected by the FBI.

sons, it can also be used to trace family relationships among males. Advancements in Y-chromosome testing may eventually eliminate the need for laboratories to extract and separate semen and vaginal cells (for example, from a vaginal swab of a rape kit) prior to analysis.

3.5 Polymerase Chain Reaction Testing – Mitochondrial DNA:

Usually, MtDNA testing is used to link a sample to a particular family since mitochondria is passed from a mother to her offspring. This type of testing can be used on extremely old or damaged samples. It can be done on samples from dried bones, teeth, hair shafts, or any other sample that contains little or highly degraded nuclear DNA . Plus which is a megaplex system developed by Perkin Elmer enabling the inspection of 10 loci and upto 36 different samples .There was a sufficient (mtDNA) analysis allows forensic laboratories to develop DNA profiles from evidence that may not be suitable for RFLP or STR analysis.

While RFLP and PCR techniques analyze DNA extracted from the nucleus of a cell, mtDNA technology analyzes DNA found in a different part of the cell, the mitochondrion .Old remains and evidence lacking nucleated cells--such as hair shafts, bones, and teeth--that are unamenable to STR and RFLP testing may yield results if mtDNA analysis is performed[27].

For this reason, mtDNA testing can be very valuable to the investigation of an unsolved case. For example, A cold case log may show that biological evidence in the form of blood, semen, and hair was collected in a particular case, but that all were improperly stored for a long period of time.

Although PCR analysis sometimes enables the crime laboratory to generate a DNA profile from very degraded evidence, it is possible that the blood and semen would be so highly degraded that nuclear DNA analysis would not yield a DNA profile. However, the hair shaft could be subjected to mtDNA analysis and thus be the key to solving the case. Finally, it is important to note that all maternal relatives (for example, a person's mother or maternal grandmother) have identical mtDNA. This

[27] See, Article on DNA Technology , Available at http://www.dna.gov/solving-crimes/cold-cases/longandshort/typesofanalysis (accessed on 12th Jan. 2007)

enables unidentified remains to be analyzed and compared to the mtDNA profile of any maternal relative for the purpose of aiding missing persons or unidentified remains investigations. Although mtDNA analysis can be very valuable to the investigation of criminal cases, laboratory personnel should always be involved in the process.

4. Sources of DNA Evidence:

Trace Evidence includes items such as hair, fibbers, paint chips, glass shards, shoe prints, gunshot residue, arson- explosives and physical matches, Baseball bat or similar weapon Handle end Sweat, skin, blood-tissue Hat, banana or mask Inside Sweat, hair, Dandruff Eyeglasses Nose or ear pieces, lens Sweat, ski Facial Tissue, Cotton swab Surface area Mucus, blood, sweat, semen, ear wax Dirty laundry Surface area Blood, Tooth-pick Tips Saliva Used cigarette Cigarette-butt Saliva Tape or ligature Inside/outside surface Skin, sweat Bottle, can, glass Sides, mouth pieces Saliva, sweat Used condoms Inside/outside surface Semen, vaginal rectal-cells Blanket, pillow, sheet Surface area Sweat, hair,, urine saliva, etc. The list is endless. Using this type of evidence, forensic scientists have been able to identify the source, only on the basis of its general appearance and structural features.

Unlike DNA, trace evidence rarely provides definitive identification. As a result, trace evidence is primarily useful only in cases that don't have DNA evidence, otherwise substantial resources can be wasted by Crime Laboratories screening for trace evidence that will not be analyzed. So, DNA evidence is more fool proof and is more reliable than trace evidence and DNA evidence can be said to produce conclusive evidence.

An investigator may collect clues for DNA test from some sources of evidences shown in the list where possibilities of existence of human cells may be there.

5. How DNA Fingerprinting is done?

5.1 Gathering DNA Evidence:

Physical evidence is any tangible object that can connect an offender to a crime scene. Biological evidence, which contains DNA, is a type of physical evidence. However,

biological evidence is not always visible to the naked eye. DNA testing has expanded the types of useful biological evidence. All biological evidence found at crime scenes can be subjected to DNA testing. Samples such as faces and vomit can be tested, but may not be routinely accepted by laboratories for testing.

5.2 Identifying DNA Evidence:

Since only a few cells can be sufficient to obtain useful DNA information to help your case, the list below identifies some common items of evidence that you may need to collect, the possible location of the DNA on the evidence, and the biological source containing the cells. Remember that just because you cannot see a stain does not mean there are not enough cells for DNA typing. Further, DNA does more than just identify the source of the sample; it can place a known individual at a crime scene, in a home, or in a room where the suspect claimed not to have been. It can refute a claim of self-defense and put a weapon in the suspect's hand. It can change a story from an alibi to one of consent. The more officers know how to use DNA, the more powerful a tool it becomes

5.3 Crime Scene Integrity:

Protection of the crime scene is essential to the protection of evidence. Safeguarding and preserving evidence is fundamental to the successful solution of a crime. Remember, while documenting evidence at the crime scene, to include descriptions of whether evidence was found wet or dry. An example of this documentation would include blood spatters.

The risk of contamination of any crime scene can be reduced by limiting incidental activity. It is important for all law enforcement personnel at the crime scene to make a conscious effort to refrain from smoking, eating, drinking, littering or any other actions which could compromise the crime scene. Because DNA evidence is more sensitive than other types of evidence, law enforcement personnel should be especially aware of their actions at the scene to prevent inadvertent contamination of evidence.

5.4 Chain of Custody:

The chain of custody of evidence is a record of individuals who have had physical possession of the evidence. Documentation is critical to maintaining the integrity of the chain of custody. Maintaining the chain of custody is vital for any type of evidence. In addition, if laboratory analysis reveals that DNA evidence was contaminated, it may be necessary to identify persons who have handled that evidence.

In processing the evidence, the fewer people handling the evidence, the better it is. There is less chance of contamination and a shorter chain of custody for court admissibility hearings.

Contamination because extremely small samples of DNA can be used as evidence, greater attention to contamination issues is necessary when identifying, collecting, and preserving DNA evidence. DNA evidence can be contaminated when DNA from another source gets mixed with DNA relevant to the case.

5.5 Transportation and Storage:

The first responding officer may be called upon to transport evidence from a crime scene. As with any evidence, the officer should ensure that the chain of custody is maintained. In addition, they should be aware that direct sunlight and warmer conditions may degrade DNA, and avoid storing evidence in places that may get hot, such as the trunk of the police car. To best preserve DNA evidence, store in a cold environment.

Any probative biological sample that has been stored dry or frozen, regardless of age, may be considered for DNA analysis. Nuclear DNA from blood and semen stains more than 20 years old has been analyzed successfully using polymerase chain reaction (PCR). Samples that have been stored wet for an extended period of time should be considered for testing only using PCR and may be unsuitable for DNA analysis. Mitochondrial DNA analysis has been performed on very old bones, teeth, and hair samples.

Samples generally considered unsuitable for testing with current techniques include embalmed bodies (with the possible exception of bone or plucked hairs), pathology or fetal tissue samples that have been immersed in formaldehyde or formalin for more than a few hours (with the notable exception of pathology paraffin blocks and slides), and urine stains. Other samples such as feces, fecal stains, and vomit can potentially be tested, but are not routinely accepted by most laboratories for testing.

5.6 Analyzing DNA Evidence:

Several basic steps are performed during DNA testing regardless of the type of test being done. The general procedure includes:

1) The isolation of the DNA from an evidence sample containing DNA of unknown origin, and generally at a later time, the isolation of DNA from a sample (e.g., blood) from a known individual;

2) The processing of the DNA so that test results may be obtained;

3) The determination of the DNA test results (or types), from specific regions of the DNA; and 4) the comparison and interpretation of the test results from the unknown and known samples to determine whether the known individual is not the source of the DNA or is included as a possible source of the DNA.

Any probative biological sample that has been stored dry or frozen, regardless of age, may be considered for DNA analysis.

Each additional test at a previously untested locus (location or site) in the DNA provides another opportunity for the result of "exclusion" if the known individual being used for comparison is not the source of the DNA from an evidence sample of unknown origin. If, however, the known individual is the source of the DNA on the evidence sample, additional testing will continue only to include that individual as a possible source of the DNA. When a sufficient number of tests have been performed in which an individual cannot be excluded as the source of the DNA by any of the tests, a point is reached at which the tests have excluded virtually the world's population and the unique identification of that individual as the source of the DNA has been achieved.

6. DNA Samples:

In the genetic finger printing technique, for carrying out DNA-test, various types of samples are used such as blood, semen, vaginal smear, body tissue, hair roots, and nasal fluid, and bone, teeth of disputes both in the civil and in the criminal justice administration. In paternity, maternity, dispute cases, rape cases, murder cases DNA test has enormous applications.

These samples are carefully collected, lawfully preserved, and properly sealed and sent to DNA Laboratory for DNA-test. Forwarding of such samples can be done in appropriate cases by the (a) learned District and Sessions Judges, Subordinate Judges, Judicial Magistrate (b) S.P., D.S.P., O/c. of Police Stations, S.I. of such Police Stations (C) Medical officers of Government Hospitals.

6.1 Bayes Theorem:

Before going further it is important to mention how exactly DNA match probabilities are represented. A statistical theorem known as Bayes Theorem is widely in use in courts and it can be represented as follows:

(Prior ODDS) x (Likelihood Ration): (Posterior Odds) which is explained in Chapter 4 with Expert Evidence[28].

In DNA profiling process firstly, the DNA is isolated from cells or tissues of the body in which the amounts of DNA found at the root of one hair is sufficient. After chemically extracting the intact DNA from the sample restriction enzymes are used to cut DNA at specific places. The DNA pieces are then sorted out according to size by sieving technique called electrophoresis in an agarose gel. The DNA fragments are blotted from the gel into a nylon membrane. This process is known as Southern Blotting. On addition of radioactive or colored probe to the nylon sheet a pattern called the DNA fingerprint is produced. The final DNA fingerprint is build by using several probes or more simultaneously.

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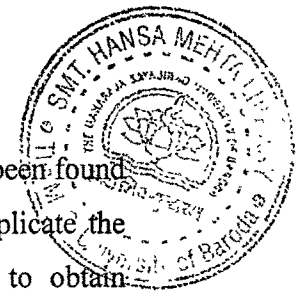
[28] Yashpal Singh and Mohammad Zaidi ,*"DNA Test in Criminal Investigation, Trial and Paternity Disputes"* , Alia Law Agency, Allahabad, 2006, p. 91



Where the samples are inadequate and the quality poor, this technique has been found to be less satisfactory. Therefore, a new technology was developed to replicate the inadequate sample, by synthesizing new DNA from the existing one to obtain sufficient quantities for analysis. This technique is called Polymerase Chain Reaction (PCR) and the testing PCR is known as PCR-STR (Short Tandem Repeat). It can produce quick, valuable results with degraded specimens In India this technique is in its infancy. Centre for DNA fingerprinting and Diagnostics (CDFD), Andhra Pradesh Forensic Science Laboratory (APFSL), Centre for Cellular and Molecular Biology (CCMB), Rajiv Gandhi Centre for Biotechnology (RGCB) are the major institutes where DNA fingerprinting is done.

6.2 Steps in DNA Sample Processing:

Each method of DNA typing has its own advantages and limitations, and each is at a different state of technical development. However, the use of each method involves three steps:-

i. Laboratory analysis of samples to determine their genetic-marker types at multiple sites of potential variation.
ii. Comparison of the genetic-marker types of the samples to determine whether the types match and thus whether the samples could have come from the same source.
iii. If the types match, statistical analysis of the population frequencies of the types to determine the probability that a match would have been observed by chance in a comparison of samples from different persons.

Before any particular DNA typing method is used for forensic purposes, precise and scientifically reliable procedures for performing all three steps must be established. It is meaningless to speak of the reliability of DNA typing in general—i.e., without specifying a particular method.

Following is a review of the steps involved in processing forensic DNA samples with STR markers. STRs are a smaller version of the VNTR sequences first described by Dr. Jeffreys. Samples obtained from crime scenes or paternity investigations are subjected to defined processes involving biology, technology, and genetics.

a. Biology:

Following collection of biological material from a crime scene or paternity investigation, the DNA is first extracted from its biological source material and then measured to evaluate the quantity of DNA recovered. After isolating the DNA from its cells, specific regions are copied with a technique known as the polymerase chain reaction, or PCR. PCR produces millions of copies for each DNA segment of interest and thus permits very minute amounts of DNA to be examined. Multiple STR regions can be examined simultaneously to increase the informativeness of the DNA test. See also Basic Biology of DNA.

b. Technology:

The resulting PCR products are then separated and detected in order to characterize the STR region being examined. The separation methods used today include slab gel and capillary electrophoresis (CE). Fluorescence detection methods have greatly aided the sensitivity and ease of measuring PCR-amplified STR alleles. After detecting the STR alleles, the number of repeats in a DNA sequence is determined, a process known as sample genotyping.

The specific methods used for DNA typing are validated by individual laboratories to ensure that reliable results are obtained and before new technologies are implemented. DNA databases, such as the one described earlier in this chapter to match Montaret Davis to his crime scene, are valuable tools and will continue to play an important role in law enforcement efforts.

c. Genetics;

The resulting DNA profile for a sample, which is a combination of individual STR genotypes, is compared to other samples. In the case of a forensic investigation, these other samples would include known reference samples such as the victim or suspects that are compared to the crime scene evidence. With paternity investigations, a child's genotype would be compared to his or her mother's and the alleged father(s) under investigation. If there is not a match between the questioned sample and the known

sample, then the samples may be considered to have originated from different sources. The term used for failure to match between two DNA profiles is 'exclusion.'

If a match or 'inclusion' results, then a comparison of the DNA profile is made to a population database, which is a collection of DNA profiles obtained from unrelated individuals of a particular ethnic group. For example, due to genetic variation between the groups, African-Americans and Caucasians have different population databases for comparison purposes.

Finally a case report or paternity test result is generated. This report typically includes the random match probability for the match in question. This random match probability is the chance that a randomly selected individual from a population will have an identical STR profile or combination of genotypes at the DNA markers tested.

i. Questioned or Unknown Samples:

Questioned or unknown samples collected from the crime scene can be any biological sample including: liquid blood or bloodstains, liquid saliva or saliva stains, and liquid semen or dried semen stains (including from vasectomies males) deposited on virtually any surface; genital/vaginal/cervical samples collected on swabs or gauze, or as aspirates; rectal/anal swabs; penile swabs; pieces of tissue/skin; fingernails; plucked and shed hairs (e.g., head, pubic, body); skin cells on drinking vessels, clothing (e.g., neck collars, waistbands, hat linings); slides containing tissue, semen, etc.; and liquid urine[29].

Samples from Unidentified Bodies:

Samples collected from unidentified bodies can include: blood, buccal swabs, hairs, bone, teeth, and fingernails, tissues from internal organs (including brain), muscle, and skin.

[29] Yashpal Singh and Mohammad Zaidi "*DNA Test in Criminal Investigation, Trial and Paternity Disputes*" , Alia Law Agency, Allahabad, 2006

ii. Reference Samples from Known Individuals:

The most common reference samples collected from known individuals are blood, oral/buccal swabs, and/or plucked hairs (e.g., head, pubic).

iii. Samples to Use When No Conventional Reference Samples Are Available:

Other samples that may be considered when individuals are unavailable or are reluctant to provide samples include clothing where biological fluids may be deposited (e.g., women's panty crotches or blood-, saliva-, or semen-stained items) and other clothing in close contact with the body where skin cells may have rubbed off (e.g., collars, waistbands, hats), bedding (with vaginal/semen stains or rubbed off skin cells), fingernail clippings, cigarette butts, toothbrushes, hairs in razors and hairbrushes, discarded facial tissues or handkerchiefs with nasal secretions, condoms, gum, feminine products, pathology paraffin blocks or slides from previous surgery or from autopsy, and teeth[30].

iv. Reference Samples from Individuals Who Have Been Transfused:

If an individual has received transfusions shortly before the collection of a blood sample (e.g., homicide victim), the DNA test results may indicate the presence of DNA from two or more sources. Generally the predominant DNA types reflect the types from the individual. However, other sources of reference samples for individuals who have received transfusions may need to be collected. These would include: blood-stained clothing or other material (bedding, etc.) and oral, vaginal, and other swabs in addition to the items listed above.

v. Use of Samples from Relatives for Testing:

Because a child inherits half of its DNA from each parent, it is possible to use reference samples collected from close relatives (e.g., biological father, mother, and/or full siblings or the individual's spouse and their children) to identify or confirm

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[30] Yashpal Singh and Mohammad Zaidi "*DNA Test in Criminal Investigation, Trial and Paternity Disputes*", Alia Law Agency, Allahabad, 2006, p. 98

the identity of bodies that have not been identified through other means. It is also possible to use reference samples collected from close relatives for comparison to crime scene samples, for example, in missing body cases where a bloodstain or tissue sample from a possible crime scene can be tested to demonstrate a biological relationship to known individuals.

vi. Determination of Paternity or Maternity of a Child or Foetus:

Aborted fetal tissue can be analyzed for determining paternity, for example, in sexual assault and/or incest cases where conception occurred. Paternity and/or maternity of a child can be confirmed using blood or other samples listed above from the child and the alleged parent(s).

6.3 Possible Results from DNA Tests:

In criminal investigations, the police collect biological evidence left at a crime scene to identify the perpetrator (and to exclude those falsely associated with an evidentiary sample). DNA typing is a powerful tool for assisting in the inculpation or exculpation of an individual as the source of biological evidence collected at the crime scene. There are three interpretations of DNA profile comparison between a known sample (e.g. a suspect) and evidentiary sample (e.g., a virginal swab continuing semen) viz.

a) Inconclusive – there is insufficient information to arrive at a conclusion.
b) Exclusive – the two DNA profiles are sufficiently different such that the sample did not originate from the same source; and,
c) Inclusive (or match) – the two DNA profiles are similar operationally and potentially could have originated from the same source.

Inclusions;

When the results obtained from the standard sample from a known individual are all consistent with or are all present in the results from the unknown crime scene sample, then the results are considered an inclusion or nonexclusion. The term "match" is also commonly used when the test results are consistent with the results from a known individual. That individual is included (cannot be excluded) as a possible source of the DNA found in the sample. Often, statistical frequencies regarding the rarity of the

particular set of genetic information observed in the unknown evidence sample and for a known individual are provided for various population groups.

It is possible for a falsely accused individual to be included as a source of a sample, particularly if the test system used only tests at one or a few loci (e.g., the DQa). In this situation, additional testing at more loci should be performed with the remaining evidence and/or DNA.

In some cases where inclusions are reported, the results are not meaningful or are inconclusive for that particular case from a legal perspective. Situations where this might apply are when the results obtained are all consistent with the individual from whom the samples were collected. [31]

Exclusion:

When the results obtained from the standard sample from a known individual are not all present in the results from the unknown crime scene sample, the results are considered exclusion, a no match, or no inclusion. With limited exceptions, an exclusion of an individual at any one genetic region eliminates that individual as a source of the DNA found in the sample.

In some cases where exclusion is reported, it may be necessary to do additional testing for that exclusion to be meaningful to the case or to provide evidence for exoneration. A situation where this might apply is when the defendant is excluded as a donor of the DNA in a sexual assault case, but no samples are available from the victim and/or consensual partners.

Inconclusive Results:

Results may be interpreted as inconclusive for several reasons. These include situations where no results or only partial results are obtained from the sample due to the limited amount of suitable human DNA or where results are obtained from an unknown crime scene sample but there are no samples from known individuals

[31] For Example. victim's results only on vaginal swabs taken from the victim, defendant's results only on a bloodstain on defendant's clothing.

available for comparison. In the latter case, the results would be suitable for comparison once an appropriate sample for comparison is tested.

Despite the challenges of forensic DNA typing, it is possible to develop reliable forensic DNA typing systems, provided that adequate scientific care is taken to define and characterize the methods.

An estimation of frequency of occurrence of a DNA profile in a general population group or groups does not arrive with the first two interpretations. However, with an 'inclusion', it is desirable to convey a valid estimate as a guideline of how common or rare the DNA profile is in the general population of potential perpetrators. To assess the rarity of a DNA profile (which ultimately assist the justice system), general population databases are generated. DNA samples from anonymous individuals from major population groups or geopolitical groups are typed for various genetic markers. The number of various forms of each marker whether they are fragment sizes, the presence or absence of dots, or specific DNA sequences, is tallied and these tallies provide a basis for estimating the rarity of DNA profiles in the various population groups.

7. Forensic Science:

According to dictionary "Forensic Science " means " relating to court or law" or "relating to court of law" in general. Forensic science includes those things or matters which are dealt with by both legal practitioners and scientists for achieving the goals of justice and for scientific inventions respectively.

The word "Forensic is taken from the Latin word "Forensic" which means something relating to court of laws or of public debate or discussion. we can say that in other word it is concerned with legal proceedings, used in judicial system for evidential purpose. In court of laws it is recognised as persuasive evidence to prove guilt or innocence of a person.

According to "Oxford companion to law Various branches of forensic science are (chemistry, physics and biology as main branch) ballistic,, blood and other biological

material, documents, photographics, serology, geology, DNA fingerprinting, brain fingerprinting, narco analysis....etc.

According to David M. walker forensic science means a branch of science concerned with the application of those bodies of knowledge for legal purpose particularly to eliciting and interpreting facts which may be of significance in legal inquiries.

It is that discipline which is directed to the recognition , identification, individualization and evaluation of physical evidence by application of the principls and methods of natural sciences for the purpose of administration of the criminal justice.

In America known as 'Public science", in France 'criminalistique", in Germany "Kriminalistik"[32].

8. Forensic Evidence:

The evidence which is accepted by scientific community and acceptable to court of laws is forensic evidence. Such evidence must pass the test of admissibility in the court according to The Indian Evidence act 1872.

9. Purpose, Use, application of DNA Fingerprinting:

- Identification of parentage: Parentage, paternity, maternity can be identified, paternity disputes
- Acceptance of parentage. : Once identified can't be denied the parentage-paternity/maternity, conclusively solve the question of maternity in case where no one ready accept the child as their biological child. Establish paternity and other family relationships
- To decide, identify, and establish the blood relation between two persons, whether they are real brother or sisters and about their grandparents.
- Where deceased is unidentified,

[32] Yashpal Singh and Mohammad Zaidi ,"*DNA Test in Criminal Investigation, Trial and Paternity Disputes*" , Alia Law Agency, Allahabad, 2006, p. 122

- For criminal investigation of murder where body is very much mutilated for identification of person and determination of the sex of the deceased.
- Used against suspects in solving various crimes.... Such as...
- Useful in mass disaster
- Identify potential suspects whose DNA may match evidence left at crime scenes
- Post conviction DNA testing - Exonerate persons wrongly accused of crimes
- Identify crime and catastrophe victims, for Criminal investigations
- Identify endangered and protected species as an aid to wildlife officials
- Could be used for prosecuting poachers
- Detect bacteria and other organisms that may pollute air, water, soil, and food
- Match organ donors with recipients in transplant programs
- Determine pedigree for seed or livestock breeds
- Authenticate consumables such as caviar and wine
- Population genetics
- Animal genetics
- Medical uses- establishing the biological relation ship of two or more persons, Organ transplantation (in medical science)
- Identifying missing children in child swapping cases, baby exchange cases
- Plant genetics
- Immigration Cases
- Identifying remains of the dead persons
- To control terrorism through preservation of genetic data in DNA data banks
- Certification and authentificaton of various food products.
- To resolve legal issues. For example, In the case of succession, inheritance of property, maintenance and adoption of minor.

10. Nature and Scope :

- DNA collection and analysis gives the criminal justice field a powerful tool for convicting the guilty and exonerating the innocent
- Only one-tenth of a single percent of DNA (about 3 million bases) differs from one person to the next. Scientists can use these variable regions to

generate a DNA profile of an individual, using samples from blood, bone, hair, and other body tissues and products.

- In criminal cases, this generally involves obtaining samples from crime-scene evidence and a suspect, extracting the DNA, and analyzing it for the presence of a set of specific DNA regions (markers).
- If the sample profiles don't match, the person did not contribute the DNA at the crime scene.
- If the patterns match, the suspect may have contributed the evidence sample.
- DNA from crime scenes also can be compared to profiles stored in a database
- DNA analysis is a powerful tool because each person's DNA is unique (with the exception of identical twins). Therefore, DNA evidence collected from a crime scene can implicate or eliminate a suspect, similar to the use of fingerprints. It also can analyze unidentified remains through comparisons with DNA from relatives. Additionally, when evidence from one crime scene is compared with evidence from other using CODIS, those crime scenes can be linked to the same perpetrator locally, statewide, and nationally.
- DNA is also a powerful tool because when biological evidence from crime scenes is collected and stored properly, forensically valuable DNA can be found on evidence that may be decades old. Therefore, old cases that were previously thought unsolvable may contain valuable DNA evidence capable of identifying the perpetrator.
- Forensic DNA typing often involves samples that are degraded, contaminated, or from multiple unknown sources. Its procedures sometimes cannot be repeated, because there is too little sample. It often involves matching of samples from a wide range of alternatives in the population and thus lacks built-in consistency checks. Except in cases where the DNA evidence excludes a suspect, assessing the significance of a result requires statistical analysis of population frequencies.

11. Use of DNA Technology in Legal Systems:

This section provides an overview of how DNA Evidence might be used in the investigation and prosecution of crimes and civil litigations. The techniques and principles behind DNA profiling are discussed in this earlier chapter. A discussion on

the issue of admissibility, in the United States and, in India in order to provide a comparative perspective is indispensable which has been discussed in the chapter of legislations. The discussion of case law is intended mainly to highlight specific issues and is not intended to be comprehensive.

In the United States there are two main tests for admissibility of scientific information from experts. One is the Frye test, enunciated in Frye v. United States[33]. The other is a 'helpfulness' standard found in the Federal Rules of Evidence and many of its State counterparts. In addition, several States in the United States have enacted laws, which essentially mandate the admission of DNA profiling evidence.

(a) The Frye Test-

The test for the admissibility of novel scientific evidence enunciated in Frye v. United States has been the most frequently invoked one in American case law. Frye lays down that the admissibility of novel scientific evidence on its general acceptance in a particular scientific field: "While Courts will go a long way in admitting expert testimony deducted from a well-recognized scientific principle or discovery, the thing from which the deduction is made must be sufficiently established to have gained general acceptance in the particular field in which it belongs. It should conduct a hearing to determine whether the scientific theory underlying the evidence is generally accepted in the relevant scientific community and to determine that the specific techniques used are reliable for their intended purpose.

In People of the State of New York v. Joseph Castro[34] the Court noted that a three-pronged test needed to be followed in determining whether the DNA evidence adduced should be admitted:

1. Is there a theory, which is generally accepted in the scientific community, which supports the conclusion that DNA forensic testing can produce reliable results?

2. Are there techniques of experiments that currently exist that are capable to producing reliable results in DNA identification and which are generally accepted in the scientific community?

[33] 293 F2d 1013 (DC Cir. 1923)
[34] 545 NYS 2d 985 Supp. Ct. 1989

3. Did the testing laboratory perform the accepted scientific techniques in analyzing the forensic samples in the case?

(b) The 'Helpless' Standard

The Federal Rules of Evidence, without specifically repudiating the Frye rule, adopt a more flexible approach, Rule 702 states that:

"If science, technical or other specialized knowledge will assist the tier of fact to understand the evidence or to determine a fact in issue, a witness qualified as an expert by knowledge, skill, experience, training or education, may testify thereto in the form of an opinion or otherwise."

Rule 702 should be read with Rule 403, which requires the court to determine the admissibility of evidence by balancing its probative force against its potential for misapplication by the jury. The Federal Rule encompasses Frye by making general acceptance of scientific principles by experts a factor, and in some cases a decisive factor, in determining probative force. A Court can also consider the qualifications of experts testifying about the news scientific principle; the use of which the new technique has been put, the technique's potential for error, the existence for specialized literature discussing the technique and its novel

The decision in Daubert v. Merrell Dow Pharmaceuticals[35] was a path breaking judgment since it modified the test laid down in Frye v. United States[36]. The scientific basis and validity of a well-known medicine for causing deformation of twins due to the consumption of his drug by the mother during pregnancy this drug was challenged. Incorporating the "helpfulness" standard in the Frye test, the following modified test was laid down:

- Has the science been tested?
- Has the science been peer reviewed and published?
- Is the science accurate?
- Is the science well accepted in the scientific community?

[35] 509 US 579 (1993)
[36] 293 F2d 1013 (DC Cir. 1923)

To produce biological evidence that is admissible in court in criminal cases, forensic investigators must be well trained in the collection and handling of biological samples for DNA analysis. They should take care to minimize the risk of contamination and ensure that possible sources of DNA are well preserved and properly identified. As in any forensic work, they must attend to the essentials of preserving specimens, labeling, and the chain of custody and must observe constitutional and statutory requirements that regulate the collection and handling of samples.[37]

In civil cases such as paternity, custody, and proof-of-death cases—the standards for admissibility must also be high, because DNA evidence might be dispositive. The relevant federal rules (Rules 403 and 702-706) and most state rules of evidence do not distinguish between civil and criminal cases in determining the admissibility of scientific data. In a civil case, however, if the results of a DNA analysis are not conclusive, it will usually be possible to obtain new samples for study.

The advent of DNA typing technology raises two key issues for judges determining admissibility and explaining to jurors the appropriate standards for weighing evidence. A host of subsidiary questions with respect to how expert evidence should be handled before and during a trial to ensure prompt and effective adjudication apply to all evidence and all experts.

In practice, the court is much more involved. The court must determine the scientific fields from which experts should be drawn. Complexities arise with DNA typing, because the full typing process rests on theories and findings that pertain to various scientific fields. For example, the underlying theory of detecting polymorphisms is accepted by human geneticists and molecular biologists, but population geneticists and other statisticians might differ as to the appropriate method for determining the population frequency of a genotype in the general population or in a particular geographic, ethnic, or other group. The courts often let experts on a process, such as DNA typing, testify to the various scientific theories and assumptions on which the process rests, even though the experts' knowledge of some of the underlying theories is likely to be at best that of a generalist, rather than a specialist.

[37] Fourth Amendment provides much of the legal framework for the gathering of DNA samples from suspects or private places, and court orders are sometimes needed in this connection.

The Frye test sometimes prevents scientific evidence from being presented to a jury unless it has sufficient history to be accepted by some subspecialty of science. Under Frye, potentially helpful evidence may be excluded until consensus has developed. By 1991, DNA evidence had been considered in hundreds of Frye hearings involving felony prosecutions in more than 40 states. The overwhelming majority of trial courts ruled that such evidence was admissible, but there have been some important exceptions.

With the helpfulness approach, the court should also consider factors that might prejudice the judge. One of the most serious concerns about scientific evidence, novel or not, is that it possesses an aura of infallibility that could overwhelm a judge's critical faculties. The likelihood that the jury would abdicate its role as critical fact-finder is believed by some to be greater if the science underlying an expert's conclusion is beyond its intellectual grasp. The judges might feel compelled to accept or reject a conclusion absolutely or to ignore evidence altogether. However, some experience indicates that jurors tend not to be overwhelmed by scientific proof and that they prefer experiential data based on traditional forms of evidence. Moreover, the presence of opposing experts might prevent a judge from being unduly impressed with one expert or the other. Conversely, the absence of an opposing expert might cause a judge to give too much weight to expert testimony, on the grounds that, if the science were truly controversial, it would have heard the opposing view. Nevertheless, if the scientific evidence is valid, the solution to those possible problems is not to exclude the evidence, but to ensure through instructions and testimony that the judge is equipped to consider rationally whatever evidence is presented.

In determining admissibility with the helpfulness approach, the court should consider a number of factors in addition to reliability. First is the significance of the issue to which the evidence is directed. If the issue is tangential to the case, the court should be more reluctant to allow a time-consuming presentation of scientific evidence that might itself confuse the judge. Second, the availability and sufficiency of other evidence might make expert testimony about DNA superfluous. And third, the court should be mindful of the need to instruct and advise the judge so as to eliminate the risk of prejudice.

11.1 Position in India:

In the Indian context, the awareness of the strength and potential of this technique is still lacking. One of the major inadequacies in this regard in this context is that this technique has not yet become a part of the Evidence Act. It is the fundamental principle of law of evidence that witnesses should state facts, which are within their knowledge, and forming of an opinion on any matter under enquiry is within the domain of the Court. However, there are situations when the Court is not in a position of form its Judgment on certain issues without the aid of persons who have acquired special skill or experience or knowledge in certain areas that are beyond the common experiences of men. When a situation like this arises, the rule is relaxed and conclusions drawn from a set of facts by especially skilled persons are admitted in evidence under the provisions of Section 45 of the Evidence Act. The judiciary looks at DNA typing as an expert witness and allows it to be admitted only under Section 45 of the Evidence Act. The present scenario in India is oscillating between two facets. The members of the forensic agencies as well as the scientific community claim that DNA fingerprinting provides a quantum leap in crime detection, while the legal fraternity on the other hand, is confused about its admissibility and application under the provisions of the Indian Evidence Act of 1872. The question of whether a suspect, or for that matter anybody, can be forced to give a blood sample for testing. The uncertainty also prevails about whether possible testing would be considered a violation of Article 20(3) of the Constitution, which protects every citizen from providing self-incriminating evidence. It has become evident in recent years, through the ruling in at least couple of important cases, that no individual can be forced to give blood samples under the existing laws. During a trial, the proponent of the evidence meets the burden of establishing that the DNA analysis performed in the present case provides a trustworthy and reliable method of identifying characteristics in an individual's genetic material.

- The following burden lies on party.
- The acquisition of the sample.
- The chain of the custody of the sample and test result.
- The proper labelling of the sample.

- The interpretation of the test results by scientist's properly qualified to read and interpret the test results.

12. Services for Laboratories:

Forensic Laboratories are the base for testing DNA evidence. The crime lab system in operation across the country varies in structure. Public crime labs may be Federal-, State-, county-, or city-sponsored. In foreign countries many public labs are associated with a law enforcement entity; some are associated with a district attorney's office, while others are independent government entities. Some forensic laboratories are privately held companies.

Not all laboratories are capable of providing comprehensive and complete forensic services. Some do not have the capability to conduct DNA testing and may need to contract out their DNA cases to other agencies or private corporations.

The functionality of each laboratory differs from the functionality of other Laboratories. The Dos and Don'ts are discussed at length in the last chapter of Thesis.

13. DNA Data Bank:

The door is opened to the possibility that this technology could be applied to forensic evidence massively. The forensic DNA analyze can be stored in a databank. It can lead to unique and unimaginable results as one can change his name, even his looks, but it is impossible to alter the DNA profile. It will confirm or deny a person's association after police investigation. In the absence of other evidence police can determine or eliminate suspects, with the help of DNA evidence. DNA databank can help in crime prevention by giving the information of potential criminals. DNA databank can be used to link crimes committed by serial offenders if both are found in a case gives a strong proof of the person's involvement. The person suspected for an unsolved crime can avoid hassle from police if voluntarily gives sample and found negative. It can apprehend the criminals just acting as eyewitness and crime recorder

of the offence, hence referred. in the offender from criminal activity. DNA data bank will reduce the time and expenditure[38].

In U.S.A. a rape and murder was solved by a match between DNA from blood and semen found at the crime scene and a databank samples from a person imprisoned for burglary. There were also various instances where some alleged persons were acquitted and proved their innocence only by the DNA test. This could not be possible without this data bank and the wonderful technique with us. Now U.S.A. and U.K. have DNA data bank legislation.

In India it is not possible to preserve DNA data of each and every person. It also violates the human rights and privacy concern. Hence it must be confined to those who are convicted in sexual offence, theft, and murder and in habit of committing these types of offences. Privacy advocates fear that samples from DNA database will be used in research aimed at identifying criminal gene. Utmost care should be taken to prevent the manipulation of the preserved data. In order to withstand the challenges of Court and to be viable in long run DNA data bank requires legislation without any human rights and privacy violation. India should come forward to draft a legislation in this regard to use DNA test as evidence under guidance of a committee of scientists, jurists, representative from the rights bodies, and security organizations such as the police and defence forces.

13.1 Forensic DNA Databases:

The development and expansion of databases that contain DNA profiles at the local, State, and national levels have greatly enhanced law enforcement's ability to solve cases with DNA. Convicted offender databases store hundreds of thousands of potential suspect DNA profiles, against which DNA profiles developed from crime scene evidence can be compared.

Given the recidivistic nature of many crimes a likelihood exists that the individual who committed the crime being investigated was convicted of a similar crime and already has his or her DNA profile in a DNA database that can be searched by the

[38] Read more in Chapter-VII about DNA Data Bank

Combined DNA Index System (CODIS) software. Moreover, CODIS also permits the cross-comparison of DNA profiles developed from biological evidence found at crime scenes. Even if a perpetrator is not identified through the database, crimes may be linked to each other, thereby aiding an investigation, which may eventually lead to the identification of a suspect.

13.2 Combined DNA Index System

CODIS[39] stands for Combined DNA Index System. It is the core of the national DNA database, established and funded by the Federal Bureau of Investigation (FBI) in U.S.A. and other countries, and developed specifically to enable public forensic DNA laboratories to create searchable DNA databases of authorized DNA profiles. The CODIS software permits laboratories throughout the country to share and compare DNA data. In addition, it provides a central database of the DNA profiles from all user laboratories. A search is conducted of the DNA profiles in this national database, known as the National DNA Index System (NDIS), and resulting matches are automatically returned by the software to the laboratory that originally submitted the DNA profile.

The term "CODIS" is often misused by law-enforcement officers, prosecutors and even practitioners of the forensic sciences when they intend to refer to a "DNA database." The index system has three levels of operation. The term "DNA database" is sometimes used without specific reference to the level, which may lead to misunderstandings. For example, some categories of profiles are allowed in a State's database but not in the National database. The term "CODIS lab" is also misused in reference to a state laboratory that does the analysis of convicted offender samples. That is a misnomer since CODIS also contain other profiles such as forensic profiles.

13.3 Basics of How CODIS Works:

CODIS uses two indexes to generate investigative leads in crimes for which biological evidence is recovered from a crime scene. The convicted offender index contains DNA profiles of individuals convicted of certain crimes ranging from certain misdemeanors to sexual assault and murder. Each State has different "qualifying

[39] CODIS is restricted DATA base, access to it and training on its use is handled by FBI, in USA.

offenses" for which persons convicted of them must submit a biological sample for inclusion in the DNA database. The forensic index contains DNA profiles obtained from crime scene evidence, such as semen, saliva, or blood. CODIS uses computer software to automatically search across these indexes for a potential match.

A match made between profiles in the forensic index can link crime scenes to each other, possibly identifying serial offenders. Based on these "forensic hits," police in multiple jurisdictions or States can coordinate their respective investigations and share leads they have developed independent of each other. Matches made between the forensic and convicted offender indexes can provide investigators with the identity of a suspect(s). It is important to note that if an "offender hit" is obtained, that information typically is used as probable cause to obtain a new DNA sample from that suspect so the match can be confirmed by the crime laboratory before an arrest is made.

13.4 Capabilities of CODIS Software

In U.S.A. The CODIS software is designed for the storage and searching of short tandem repeat (STR) profiles. The same version of the software is used by all participating laboratories at the local, state, and federal levels. Although the main version of CODIS is for handling STR results, a separate version exists for the entry and searching of mitochondrial DNA (mtDNA) profiles.

The four primary functions of the CODIS software are:

- DNA profile entry and management: the function dealng with the database DNA profiles.
- Searching: the function allowing a search of database DNA profiles.
- Match management: the function managing search results. For example, it allows a laboratory to record and distinguish whether a particular match is an offender hit or a forensic hit, and whether the match is within or outside of the state.
- Statistical calculations: the function enabling laboratory personnel to calculate profile statistics, based on the laboratory's or FBI's population frequency data.

- The FBI in U.S.A. provides CODIS software40 to all public forensic laboratories at no cost. However, the cost of the computer hardware and all support software is the laboratory's responsibility. Upgrades and technical support of the software is also provided free to all laboratories. Copies of CODIS software provided to some foreign countries are stand-alone copies not connected to the CODIS network in the United States.

13.5 Levels of the Database:

The National DNA Index System (NDIS) is a system of DNA profile records input by criminal justice agencies (including State and local law enforcement agencies). The Combined DNA Index System (CODIS) is the automated DNA information processing and telecommunication system that supports NDIS.

i. Local:

A local laboratory can maintain its own local database of forensic profiles—local DNA index system (LDIS)—and upload approved profiles to SDIS.

ii. State:

The state database, or State DNA index system (SDIS), contains forensic profiles from local laboratories in that state, plus forensic profiles analyzed by the state laboratory itself. The state database also contains DNA profiles of convicted offenders. States may have their own regulations regarding which profile types can be maintained at SDIS.

iii. National:

Profiles from the states (including the FBI) are uploaded into the National DNA Index System (NDIS). In accordance with Federal law, specific rules govern whether a profile can or cannot be uploaded to NDIS Some categories of samples, as well as DNA profiles that do not meet minimum number of DNA loci, are not eligible for entry into NDIS. Approved analysts should familiarize themselves with NDIS Board procedures.

[40] See relevant sections of the Federal Law of U.S.A.,"Justice For All Act 2004", relating to CODIS

13.6 NDIS Procedures and Administration in U.S.A.:

(In India we can adopt under mentioned mechanism for formulating the CODIS at state and central level.)

Each state is responsible for determining its own policies regarding samples allowed in the state's DNA database, primarily via legislation regarding the creation and use of DNA databases. Each state can set its own policies, data entry, and/or search schedules, and other activities on CODIS within that state. However, there is still an expectation of reasonable uniformity amongst states about the use of CODIS.

The NDIS Procedures Board is responsible for development and modification of policy regarding NDIS use. Board membership comprises representatives of Central, state, and local laboratories. State or local laboratories that contribute DNA profiles to NDIS must comply with NDIS procedures, posted on the CJIS-WAN CODIS website. NDIS procedures provide details regarding acceptance of DNA profiles at the national level. One requirement, for example, is that a forensic evidence DNA profile must have results at 10 or more of specific CODIS core loci.

Each laboratory is required to designate a CODIS Administrator, who is responsible for CODIS data and serves as the primary point of contact for CODIS issues in that laboratory. Each state has a designated CODIS State Administrator, who serves as the state's CODIS point of contact and is responsible for coordinating and communicating with all CODIS administrators in the state's local laboratories regarding CODIS issues. CODIS state administrators also serve as gatekeepers for entering data from states into NDIS. While preparing CODIS following things are required to be considered[41].

- Legal developments and procedures.
- CODIS software upgrades and modifications.
- Exchange of information and CODIS experiences.
- Formulation and clarification of CODIS policies and NDIS procedures.
- CODIS software modification and improvements.

[41] Yashpal Singh and Mohammad Zaidi, *"DNA Test in Criminal Investigation, Trial and Paternity Disputes"*, Alia Law Agency, Allahabad, 2006, p. 59

- Issues relating to CODIS and DNA databases.

The working group also addresses CODIS issues directed to its attention by the NDIS Procedures Board or the SWGDAM chairman. The board and working group comprises members who are CODIS users at the local, state, or national level.

13.7 Forensic databases:

Forensic databases are organized bodies of information that can be accessed on certain criteria. Forensic databases consist of:

a) A convicted offender database
b) An unsolved cases (or not available suspect cases)
c) Population frequency databases, and
d) Missing person database.

The DNA database contains information about DNA profile, identifiers for the laboratory examiner, case sample and population statistics.

(a) Convicted Offender Database:

It consists of DNA profiles from known individuals convicted of crimes for which the deposition of biological materials by a suspect is likely (e.g., example homicide, attempted homicide, sexual assault, kidnapping assault). A biological sample, which may be a liquid blood or buckle sample, is collected at the time of incarceration or before the convicted offender is released. Dried replicate specimens are prepared and frozen in a restricted access facility in case future analysis is required. A portion of each donors sample is subjected to analyses against genetic loci known to be forensically informative. Typing information (e.g., ban size, numerical type designation) is then determined and entered into the database with the appropriate identifying information (e.g., sample numbers) to permit only simple identification and retrieval.

(b) Unsolved Cases Database:

DNA profile that can be contained in forensic database may include there from semen left behind at an unsolved rape, blood typed on knife found at the scene of a homicide that did not come from victim, or hair not originating from a victim other known person who had access to this scene.

(c) Population Database:

This is a depository of population statistics information often used to study on how frequently forensically, important genetic markers occur among various geographic areas or community and ethnic groups. Population databases are necessary to validate an estimate of how rare a DNA profile is. The identity of donor of individual samples is not carried within the population databases; generally the source of each sample is anonymous.

(d) Missing Person Database and Unidentified Decedents:

The information includes the DNA profiled derived from body parts whose origin is unknown and profiles from parents or children of missing persons.

For criminal investigation purpose we can further bifurcate profiles as under:

(e) Forensic Profiles:

Significant numbers of forensic profiles entered by states into CODIS are probative profiles from cases where the perpetrator is not known, commonly referred to as unsolved cases. Additionally, states also enter forensic evidence profiles that match the reference profile of the suspect in that case (solved cases). Forensic profiles are entered into CODIS in the hope that a match will result from a search of the database, and an investigative lead generated.

(f) Arrestee Profiles:

States can collect DNA samples from individuals arrested for certain offences and maintain those DNA profiles in an arrestee database. In those states, specific laws

require individuals arrested for qualifying offenses to provide a DNA sample for the database. States may upload these profiles to NDIS.

(g) Suspect Profiles:

The states can also maintain a suspect database, containing suspects' reference profiles lawfully collected in connection with criminal cases. These profiles are ineligible for upload into NDIS.

(h) DNA Identification in Mass Fatality Incidents[42]

DNA analysis is the gold standard for identification of human remains from mass disasters. Particularly in the absence of traditional anthropological and other physical characteristics, forensic DNA typing allows for identification of any biological sample and the association of body parts, as long as sufficient DNA can be recovered from the samples. This is true even when the victim's remains are fragmented and the DNA is degraded.

Unidentified Human remains, missing persons and relative of missing person Profiles:[43] Some states in United States also enters unidentified human remains, missing person or remains of missing persons profile into CODIS. It includes results from mtDNA analysis as well as STR profiles.

It is advocated for a comprehensive statute legalizing the DNA profiling system is necessary and needs to provide for –

1. The Authority to establish databases
2. The declared purpose of the use of databases
3. Who can and cannot be subjected to sample collections
4. What offences are covered?
5. The types of samples so collected and by whom

[42] The examples of mass disaster are : 9/11 attacks of the World Trade Centere,Hurrican Katrina,,South East Tsunami, killari and Gujarat 2001 earth quack

[43] See,details discussion of all these issues in "lesson learned from 9/11:DNA identification in mass Fatality accident .An excessive overview of forensic identification beyond DNA analysis can be found in Mass fatality incidents. A guide for human forensic identification,U.S. Department of Justice, National Institute of Justice, June 2005

6. The assignment of responsibility for the collection, maintenance and administration of the database records
7. Unauthorized use of DNA databases and penalties for that unauthorized use
8. Provisions for the impingement DNA data from such an archive an
9. Specifications for the unauthorized disclosure of DNA records

Evidentiary Perspective:

- All profile data can be digitally and numerically stored in a computer.
- The database can be readily retrieved and compared with evidentiary profiles. Although comparisons of DNA profile can be made within a case or among profiles a database, the quality issues are slightly different. In a particular case, when comparing, for example, a suspect's profile with that of evidence sample, one is more concerned with the false-positive scenario (i.e., that one or both of the samples have been typed incorrectly and a match has resulted when the samples are genetically different at those markers).
- Laboratories practice standards protocols to minimize the occurrence of false positive, samples can usually be reanalyzed. A false-negative scenario is more tolerated in a particular case because it would not result in wrongly inculpating an individual. In contrast, for a database search for potential matching profiles to be effective, a false – negative result is less tolerated. If matches cannot be made in a database, where matches exist, then there would be no need to generate databases for identifying repeat offenders or serial perpetrators.
- A false positive can be eliminated in database search by requiring re-analysis of the known samples by the querying laboratory. Establishing validated and robust protocols and establishing proper guidelines for quality assurance and control can minimize a false negative.

In USA, DNA typing standards were created by DNA Advisory Board (DAB) by the DNA Identification Act of 1994. DAB is responsible for promulgating national standards of forensic data analysis.

DAB addressed issues as:

1) laboratory organizations,
2) personal qualification, (3)documentation,
3) materials and equipments
4) validation of analytical procedures,
5) generation and validation of genetic marker frequency databases
6) evidence handling procedures,
7) internal controls and standards,
8) Data analysis and reporting,
9) proficiency testing,
10) Quality audit and safety.
11) Training and Assistance
12) Educational Materials for Families
13) Research, Development, and Testing
14) Funding for Crime Laboratories

Since the inception of forensic DNA profiling considerable benefits have been gained from integrating information management and communication technologies with the data derived from forensic DNA analysis. The Establishment of various forensically useful databases, for both population and forensic data was also recognized as pivotal to the process of resolving crimes where there is no suspect or multiple crimes that may be committed by the same individual. N 1989, the FBI created 'Combined DNA Index System' (CODIS), since then CODIS is serving a powerful tool for the use in forensic DNA profiling in generating investigative leads. Most forensic DNA laboratories have built their respective DNA analysis programmes in four areas:-

1. Case Work;
2. Research and Development of Technology;
3. Technology and Data Sharing; and
4. A computerized indexing system.

In USA, NDIS is statutorily authorized to disclose information to criminal justice agencies participating in investigation in respect of an identification match only[44].

1. To criminal justice agencies for purposes of law enforcement identification.
2. In judicial proceedings, if otherwise admissible pursuant to applicable statute and rules.
3. For Criminal defence purposes to a defendant who shall have access to sample and analyses performed in connection with the case in which the defendant is charged.
4. If personally identifiable information is removed; for a population statistics database, for identification research and protocol development, or for quality control purposes.

14. DNA Laboratories:

DNA Laboratory is a place where DNA evidence is collected, stored, preserve, labbeled and administered by the government Authorities, especially in U.S.A, U.K. and other countries enforced by law and legislative force. In India there are some Labs working on the same guidelines, but still there is a need of formulating laws to introduce nation wide centrally controlled laboratory system with uniformity.

Reliable and accurate results are a national concern for crime laboratories. Decisions about guilt or innocence are made based on a laboratory's analysis of evidence. Additionally, demands on crime laboratories change consistently with new technologies, legislation, and needs of the criminal justice field. Laboratory Services include

- Lab Audits
- Grant Progress Assessments
- Sample Analysis
- Accreditation Assistance And Quality Documentation
- DNA Sample Analysis
- DNA Laboratory Audits And Accreditation
- DNA Sample Collection Kits

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[44] Yashpal Singh and Mohammad Zaidi ,*"DNA Test in Criminal Investigation, Trial and Paternity Disputes"* , Alia Law Agency, Allahabad, 2006, p. 51

- Quality Documents
- Expert Systems Tested Project
- Sequencing Unusual Str Alleles
- Validation Information For Labs
- Us Y-Str Database DNA Sample Analysis
- Quality Assurance Standards For Forensic DNA Testing Laboratories (FBI)

In U.S.A. the crime lab systems in operation across the country vary in structure. Public crime labs may be Federal-, State-, county-, or city-sponsored. Many public labs are associated with a law enforcement entity; some are associated with a district attorney's office, while others are independent government entities. Some forensic laboratories are privately held companies.

Not all laboratories are capable of providing comprehensive and complete forensic services. Some do not have the capability to conduct DNA testing and may need to contract out their DNA cases to other agencies or private corporations.

Not all laboratories are capable of the same DNA testing either. Most DNA labs have the capability to conduct testing on nuclear DNA, which is the single copy of DNA that exists in every cell nucleus. A select few specialize in Y-STR testing, which is DNA conducted on the Y-chromosome, which is found only in males. Others specialize in testing mitochondrial DNA (or mtDNA), which is found in every cell of the body regardless of the presence of a nucleus.

Concerns over the Privacy and Confidentiality of Forensic and Medical Genetic Data Banking:

Confidentiality and security of DNA-related information are especially important and difficult issues, because we are in the midst of two extraordinary technological revolutions that show no signs of abating.

Forensically DNA Profiling has more efficient scientific usage, but there is an imminent need to balance the benefits of genetic information to society particularly medical and forensic realms, with the right of individuals to control information about them and prevent its use for information about them and prevent its use for purposes

other than those for which it was created. Balancing between molecular biology, which is yielding an explosion of information about human genetics, and in computer technology, which is moving toward national and international networks connecting growing information resources is also very important

- The potential sensitivity of DNA information and the digital information management system for storage of large number of data and quick retrieval calls for effective interlocking and control measures by the system users.
- Forensic applications of DNA technology revolving with stringent privacy consideration of controls in mind and the forensic community have addressed a number of potential privacy issues.
- The predisposition of a donor to no one or more genetically induced conditions is generally not retrievable from forensic genetic data; only the potential for the individualization of donor to the exclusion of all others (or an exclusion as the source of the evidence sample) by the genetic information can be obtained.
- Medically sensitive information cannot be derived from forensic DNA analysis. The genetic information used in forensic DNA typing is well established and known by the scientifically forensic and legal community.
- The limited dissemination of forensic DNA information to authorized recipients during Court proceedings or pre-trial activities has no medical or other values.
- Investigative information as to the nature of the crime is often provided to the forensic analyst so that the proper analysis can be performed and information and conclusion about leads can be derived; but the information is not directly associated with the samples themselves and therefore would not be a part of the database.
- Sensitive identifying information about a donor (e.g., social security number) has no bearing on a value to the forensic analytical process. Submissions of evidence are usually identified by a unique sequential number (e.g., year, month, date and order issued) or alphanumeric generated by the laboratory and, perhaps contributing agency. Simple designator (often alphanumeric) are assigned to individual specimens and used for efficiency during the analysis.

- Forensic laboratories and police are subject to strict legal and procedural requirement, as to the chain of custody of the physical evidence (i.e., source of genetic information) and the release of information to unauthorized, personnel. Forensic laboratories are restricted access facilities, making unauthorized access difficult.
- The authorizations to collect, preserve, and analyze sample to be contained with such a database, and the restrictions and limitation of such uses including privacy and confidentiality issues and penalties for violation, are created by a legislative body with associated legal review, scientific comment and recommendations. This becomes part of the public record.
- The computer technology required for an automated fingerprint identification system is sophisticated and complex.
- Fingerprints are complicated geometric patterns, and the computer must store, recognize, and search for complex and variable patterns of ridges and minutiae in the millions of prints on file. Several commercially available but expensive computer systems are in use around the world.
- In contrast, the computer technology required for DNA databanks is relatively simple. Because DNA profiles can be reduced to a list of genetic types (hence, a list of numbers), DNA profile repositories can use relatively simple and inexpensive software and hardware. Consequently, computer requirements should not pose a serious problem in the development of DNA profile databanks. Confidentiality and security of DNA related information are especially difficult and important issues, because we are in the mids of two extraordinary technological revolutions that shows n o sings of abating: in molecular biology , which is yielding an explosion of information about human genetics, and in computer technology, which is moving towards national and international networks connecting growing information resources.
- Even simple information about identity requires confidentiality. Just as fingerprint files can be misused, DNA profile information could be misused to search and correlate criminal-record databanks or medical-record databanks.
- Computer storage of information increases the possibilities for misuse. For example, addresses, telephone numbers, social security numbers, credit ratings, range of incomes, demographic categories, and information on

hobbies are currently available for many of our citizens in various distributed computerized data sources. Such data can be obtained directly through access to specific sources, such as credit-rating services, or through statistical disclosure, which refers to the ability of a user to derive an estimate of a desired statistic or feature from a databank or a collection of databanks.

- Disclosure can be achieved through one query or a series of queries to one or more databanks. With DNA information, queries might be directed at obtaining numerical estimates of values or at deducing the state of an attribute of an individual through a series of Boolean (yes-no) queries to multiple distributed databanks.
- Several private laboratories in U.S.A. already offer a DNA-banking service (sample storage in freezers) to physicians, genetic counsellors, and, in some cases, anyone who pays for the service. Typically, such information as name, address, birth date, diagnosis, family history, physician's name and address, and genetic counsellor's name and address is stored with samples. That information is useful for local, independent bookkeeping and record management. But it is also ripe for statistical or correlative disclosure. Just the existence in a databank of a sample from a person, independent of any DNA-related information, may be prejudicial to the person.
- In some laboratories, the donor cannot legally prevent outsiders' access to the samples, but can request its withdrawal. A request for withdrawal might take a month or more to process. In most cases, only physicians with signed permission of the donor have access to samples, but typically no safeguards are taken to verify individual requests independently. That is not to say that the laboratories intend to violate donors' rights; they are simply offering a service for which there is a recognized market and attempting to provide services as well as they can.

Following are few suggestions to avoid all above mentioned problems:

- In the future, if pilot studies confirm its value, a national DNA profile databank should be created that contains information on felons convicted of particular violent crimes. Among crimes with high rates of recidivism, the case is strongest for rape, because perpetrators typically leave biological

evidence (semen) that could allow them to be identified. Rape is the crime for which the databank will be of primary use. The case is somewhat weaker for violent offenders who are most likely to commit homicide as a recidivist offence, because killers leave biological evidence only in a minority of cases.

- The databank should also contain DNA profiles of unidentified persons made from biological samples found at crime scenes. These would be samples known to be of human origin, but not matched with any known persons.
- Databanks containing DNA profiles of members of the general population (as exist for ordinary fingerprints for identification purposes) are not appropriate, for reasons of both privacy and economics.
- DNA profile databanks should be accessible only to legally authorized persons and should be stored in a secure information resource.
- Legal policy concerning access and use of both DNA samples and DNA databank information should be established before widespread proliferation of samples and information repositories. Interim protection and sanctions against misuse and abuse of information derived from DNA typing should be established immediately. Policies should explicitly define authorized uses and should provide for criminal penalties for abuses.
- Although the committee endorses the concept of a limited national DNA profile databank, it doubts that existing RFLP-based technology provides an appropriate wise long-term foundation for such a databank. We expect current methods to be replaced soon with techniques that are simpler, easier to automate, and less expensive—but incompatible with existing DNA profiles. Accordingly, the committee does not recommend establishing a comprehensive DNA profile databank yet.
- For the short term, we recommend the establishment of pilot projects that involve prototype databanks based on RFLP technology and consisting primarily of profiles of violent sex offenders. Such pilot projects could be worthwhile for identifying problems and issues in the creation of databanks. However, in the intermediate term, more efficient methods will replace the current one, and the forensic community should not allow itself to become locked into an outdated method.

- State and federal laboratories, which have a long tradition and much experience in the management of other types of basic evidence, should be given primary responsibility, authority, and additional resources to handle forensic DNA testing and all the associated sample-handling and data-handling requirements.
- Private-sector firms should not be discouraged from continuing to prepare and analyze DNA samples for specific cases or for databank samples, but they must be held accountable for misuse and abuse to the same extent as government-funded laboratories and government authorities.
- In U.S.A. the partner agencies of the DNA Initiative are working to help ensure that DNA forensic technology is used to its full potential to identify missing persons by providing:
- Nihil Simul Inventum Est Et Perfactum – A Thing Invented Takes Time To Be Perfected

Thus it can be concluded that because of the reasons such as Discrimination potential, Sensitivity, Reliability, Ease of interpretation, Speed of analysis and Cost effectiveness the DNA Technology shall be utilised in various fields, especially investigation.